



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 102806**

**TO: Minh-Tam Davis**  
**Location: CM1/8A01&8E12**  
**Art Unit: 1642**

*Sept 6*, 2003

**Case Serial Number: 09/700700**

**From: P. Sheppard**  
**Location: CM1-1E03**  
**Phone: (703) 308-4499**

**sheppard@uspto.gov**

### **Search Notes**

**THIS PAGE BLANK (USPTO)**

From: Chan, Christina  
Sent: Saturday, August 30, 2003 9:39 AM  
To: Davis, Minh-Tam; STIC-Biotech/ChemLib  
Subject: RE: Rush search request for 09/700700

Please ~~rush~~: Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644  
308-3973  
CM-1, 9B19

-----Original Message-----

From: Davis, Minh-Tam  
Sent: Friday, August 29, 2003 10:49 AM  
T : Chan, Christina  
Subject: Rush search request for 09/700700

1) Please search SEQ ID NO:335 in the following parent cases of 09/439313 for priority date determination.

09439313 <snquery.pl?APPL\_ID=09439313>

is a continuation in part of 09352616 <snquery.pl?APPL\_ID=09352616>

Which is a continuation in part of 09288946 <snquery.pl?APPL\_ID=09288946>

Which is a continuation in part of 09232149 <snquery.pl?APPL\_ID=09232149>

Which is a continuation in part of 09159812 <snquery.pl?APPL\_ID=09159812>

Which is a continuation in part of 09115453 <snquery.pl?APPL\_ID=09115453>

Which is a continuation in part of 09030607 <snquery.pl?APPL\_ID=09030607>

Which is a continuation in part of 09020956 <snquery.pl?APPL\_ID=09020956>

Which is a continuation in part of 08904804 <snquery.pl?APPL\_ID=08904804>

Which is a continuation in part of 08806099 <snquery.pl?APPL\_ID=08806099>

? leave # 335  
to 7/14/98 file date  
Same as # 115  
Leave both file 2/25/98  
part of # 335  
do not leave any  
part of # 335

1) Please search SEQ ID NO:1 of the instant application against the sequences of 20030022275 (or US 6617129) and 60/051080

Thank you.

MINH TAM DAVIS

ART UNIT 1642, ROOM 8A01, MB 8E12

305-2008

11  
STN = 09/105,470

Point of Contact  
P. Sheppard  
telephone number: (703) 308-4499

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: 9/6/03  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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[illegible]

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[illegible]





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1010 1020 1030 1040 1050 1060 1070 1080 1090 1100

1110 1120 1130 1140 1150 1160 1170 1180 1190 1200

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1310 1320 1330 1340 1350 1360 1370 1380 1390 1400

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2410 2420 2430 2440 2450 2460 2470 2480 2490 2500

2510 2520 2530 2540 2550 2560 2570 2580 2590 2600

2610 2620 2630 2640 2650 2660 2670 2680 2690 2700

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2810 2820 2830 2840 2850 2860 2870 2880 2890 2900

2910 2920 2930 2940 2950 2960 2970 2980 2990 3000

3010 3020 3030 3040 3050 3060 3070 3080 3090 3100

3110 3120 3130 3140 3150 3160 3170 3180 3190 3200

3210 3220 3230 3240 3250 3260 3270 3280 3290 3300

3310 3320 3330 3340 3350 3360 3370 3380 3390 3400

3410 3420 3430 3440 3450 3460 3470 3480 3490 3500

3510 3520 3530 3540 3550 3560 3570 3580 3590 3600

3610 3620 3630 3640 3650 3660 3670 3680 3690 3700

3710 3720 3730 3740 3750 3760 3770 3780 3790 3800

3810 3820 3830 3840 3850 3860 3870 3880 3890 3900

3910 3920 3930 3940 3950 3960 3970 3980 3990 4000

4010 4020 4030 4040 4050 4060 4070 4080 4090 4100

4110 4120 4130 4140 4150 4160 4170 4180 4190 4200

4210 4220 4230 4240 4250 4260 4270 4280 4290 4300

4310 4320 4330 4340 4350 4360 4370 4380 4390 4400

4410 4420 4430 4440 4450 4460 4470 4480 4490 4500

4510 4520 4530 4540 4550 4560 4570 4580 4590 4600

4610 4620 4630 4640 4650 4660 4670 4680 4690 4700

4710 4720 4730 4740 4750 4760 4770 4780 4790 4800

4810 4820 4830 4840 4850 4860 4870 4880 4890 4900

4910 4920 4930 4940 4950 4960 4970 4980 4990 5000

5010 5020 5030 5040 5050 5060 5070 5080 5090 5100

5110 5120 5130 5140 5150 5160 5170 5180 5190 5200

5210 5220 5230 5240 5250 5260 5270 5280 5290 5300

5310 5320 5330 5340 5350 5360 5370 5380 5390 5400

5410 5420 5430 5440 5450 5460 5470 5480 5490 5500

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5610 5620 5630 5640 5650 5660 5670 5680 5690 5700

5710 5720 5730 5740 5750 5760 5770 5780 5790 5800

5810 5820 5830 5840 5850 5860 5870 5880 5890 5900

5910 5920 5930 5940 5950 5960 5970 5980 5990 6000

6010 6020 6030 6040 6050 6060 6070 6080 6090 6100

6110 6120 6130 6140 6150 6160 6170 6180 6190 6200

6210 6220 6230 6240 6250 6260 6270 6280 6290 6300

6310 6320 6330 6340 6350 6360 6370 6380 6390 6400

6410 6420 6430 6440 6450 6460 6470 6480 6490 6500

6510 6520 6530 6540 6550 6560 6570 6580 6590 6600

6610 6620 6630 6640 6650 6660 6670 6680 6690 6700

6710 6720 6730 6740 6750 6760 6770 6780 6790 6800

6810 6820 6830 6840 6850 6860 6870 6880 6890 6900

6910 6920 6930 6940 6950 6960 6970 6980 6990 7000

7010 7020 7030 7040 7050 7060 7070 7080 7090 7100

7110 7120 7130 7140 7150 7160 7170 7180 7190 7200

7210 7220 7230 7240 7250 7260 7270 7280 7290 7300

7310 7320 7330 7340 7350 7360 7370 7380 7390 7400

7410 7420 7430 7440 7450 7460 7470 7480 7490 7500

7510 7520 7530 7540 7550 7560 7570 7580 7590 7600

7610 7620 7630 7640 7650 7660 7670 7680 7690 7700

7710 7720 7730 7740 7750 7760 7770 7780 7790 7800

7810 7820 7830 7840 7850 7860 7870 7880 7890 7900

7910 7920 7930 7940 7950 7960 7970 7980 7990 8000

8010 8020 8030 8040 8050 8060 8070 8080 8090 8100

8110 8120 8130 8140 8150 8160 8170 8180 8190 8200

8210 8220 8230 8240 8250 8260 8270 8280 8290 8300

8310 8320 8330 8340 8350 8360 8370 8380 8390 8400

8410 8420 8430 8440 8450 8460 8470 8480 8490 8500

8510 8520 8



Residue Identity = 99% Match

Initial score	=	2/8	Optimized Score	=	364	Significance	=	2.06
Residue Identity	=	.99%	Matches	=	365	Mismatches	=	1
Gaps	=	2	Conservative Substitutions	=			=	0

TELEFAX: (206) 682-6031

2 ID NO 115

SOFTWARE: FABLESEY FOR WINDOWS VERSION 3.0  
 SEQ ID NO 115

AAATTAATTCTTCACTTGGAATTGACAGGATTCACACTTTACGTGATGATATATTGGTGCAAAAA  
2540 2550 2560 2570 2580 2590 2600

2680 2690 2700 2710 2720 2730 2740

TTGGTTCAGAACCATTCACCCAGACAGCCTGTTCTATCCTGTTAATAATTAGTTGGGTTCTCTACA



240 250 260 270 280 290 300  
 2830 2840 2850 2860 2870 2880 2890  
 TGCATACAAACCCCTGCTCAATCTGTCATCAATAAAGTGTGACTGATAATTAGTAGAGACCCCAACCA  
 TGATACAAACCCCTGCTCAATCTGTCATCAATAAAGTGTGACTGATAATTAGTAGAGACCCCAACCA  
 310 320 330 340 350 360 X  
 2900 2910 2920  
 ACTTATTTTCTGATGTGTTTTCACATATGAG

## 13. US-09-439-313-335 (1-2984)

US-09-030-607-20 Sequence 207, Application US/09030607

Sequence 207, Application US/09030607

Patent No. 6262245

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO

NUMBER OF SEQUENCES: 224

CORRESPONDENCE ADDRESSES:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/030,607

FILING DATE: 25-FEB-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.427C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 207:

SEQUENCE CHARACTERISTICS:

LENGTH: 332 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: CDNA

Initial Score = 253 Optimized Score = 318 Significance = 1.84

Residue Identity = 96% Matches = 322 Mismatches = 7

Gaps = 4 Conservative Substitutions = 0

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 CCAAAAGCTTATCTGCTTGAATTTTAAAGTTGGGGGAGATTCGATTCGATTAAGACATGCA  
 1620 1630 1640 1650 1660 1670 1680  
 TTTTAAAGCTGACACTCTTATTTCTTCCCTTAAATATATGATTAATCCCAATCTATTAAAG  
 TTTTAAAGCTGACACTCTTATTTCTTCCCTTAAATATATGATTAATCCCAATCTATTAAAG  
 30 40 50 60 70 80 90  
 1690 1700 1710 1720 1730 1740 1750  
 ACTGACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGAGTTCCTGCTTATGAGTCAAGT  
 ACTGACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGAGTTCCTGCTTATGAGTCAAGT

100 110 120 130 140 150 160  
 1760 1770 1780 1790 1800 1810 1820 1830  
 TGACATCTCTTGAGAAATCTTGTGATGAGAGAGTGAAGATTTGATTTTCACAGAGGAAGAACAGC  
 TGACATCTCTTGAGAAATCTTGTGATGAGAGAGTGAAGATTTGATTTTCACAGAGGAAGAACAGC  
 170 180 190 200 210 220 230  
 1840 1850 1860 1870 1880 1890  
 GCAG-AATGAA-GGGCCAGCTTACTGAGC-TGTCCAGTGAAGAGCTTCAATGGTGGACATGGAAGAAG  
 GCAGAAATGAAGGGGCCAGCTTACTGAGC-TGTCCAGTGAAGAGCTTCAATGGTGGACATGGAAGAAG  
 240 250 260 270 280 290 300  
 1900 1910 1920 X 1930 1940 1950 1960 1970  
 CAGCTTGGCCCTGGGAGAGCCGATCCTGAGCAAGAGGAGTGAAGTGTGAGCAAGAAAGGCT  
 CAGCTTGGCCCTGGGAGAGCCGATCCTGAGCAAGAGGAGTGAAGTGTGAGCAAGAAAGGCT  
 310 320 330 X

A

## 14. US-09-439-313-335 (1-2984)

US-09-352-616A-2 Sequence 207, Application US/09352616A

Sequence 207, Application US/09352616A

Patent No. 6395278

GENERAL INFORMATION:

APPLICANT: Dillon, Davin C.

APPLICANT: Harlocker, Susan Louise

APPLICANT: Jiang, Yuqi

APPLICANT: Xu, Jiangchun

APPLICANT: Mitcham, Jennifer Lynn

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

FILE REFERENCE: 210121.427C8

CURRENT APPLICATION NUMBER: US/09/352,616A

CURRENT FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 472

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 207

LENGTH: 332

TYPE: DNA

ORGANISM: Homo sapien

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)..(332)

OTHER INFORMATION: n = A,T,C or G

Initial Score = 253 Optimized Score = 318 Significance = 1.84  
 Residue Identity = 96% Matches = 322 Mismatches = 7  
 Gaps = 4 Conservative Substitutions = 0

1550 1560 1570 1580 1590 X 1600 1610  
 CCAAAAGCTTATCTGCTTGAATTTTAAAGTTGGGGGAGATTCGATTCGATTAAGACATGCA  
 1620 1630 1640 1650 1660 1670 1680  
 TTTTAAAGCTGACACTCTTATTTCTTCCCTTAAATATATGATTAATCCCAATCTATTAAAG  
 TTTTAAAGCTGACACTCTTATTTCTTCCCTTAAATATATGATTAATCCCAATCTATTAAAG  
 30 40 50 60 70 80 90  
 1690 1700 1710 1720 1730 1740 1750  
 ACTGACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGAGTTCCTGCTTATGAGTCAAGT  
 ACTGACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGAGTTCCTGCTTATGAGTCAAGT

100 110 120 130 140 150 160  
 1690 1700 1710 1720 1730 1740 1750  
 ACTGACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGAGTTCCTGCTTATGAGTCAAGT  
 ACTGACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGAGTTCCTGCTTATGAGTCAAGT



1760 1770 1780 1790 1800 1810 1820 1830  
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGGAACACAGC  
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGGAACACAGC  
 170 180 190 200 210 220 230  
 1840 1850 1860 1870 1880 1890  
 GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGAAGGCTCATGGTGGACATGAAAGAGG  
 GCAGAAATGAAGGGCCAGGCTTACTGAGC-TGTCCAGTGAAGGCTCATGGTGGACATGAAAGAGG  
 240 250 260 270 280 290 300  
 1900 1910 1920 X 1930 1940 1950 1960 1970  
 CAGCTTAGGCCCCCTGGGGAGCCAGTCCACTGAGCAAGAGGACTGAGCCTTTTGCAGAAAGGCT  
 CAGCTTAGGCCCCCTGGGGAGCCCA  
 310 320 330 X

A

15. US-09-439-313-335 (1-2984)  
 US-09-232-149A-2 Sequence 207, Application US/09232149A

Sequence 207, Application US/09232149A  
 Patent No. 6465611  
 GENERAL INFORMATION:  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer Lynn  
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE  
 TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE  
 FILE REFERENCE: 210121.427C6  
 CURRENT APPLICATION NUMBER: US/09/232,149A  
 CURRENT FILING DATE: 1999-01-15  
 NUMBER OF SEQ ID NOS: 338  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 207  
 LENGTH: 332  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)..(332)  
 OTHER INFORMATION: n = A,T,C or G  
 Initial Score = 253 Optimized Score = 318 Significance = 1.84  
 Residue Identity = 96% Matches = 322 Mismatches = 7  
 Gaps = 4 Conservative Substitutions = 0

1550 1560 1570 1580 1590 X 1600 1610  
 CCCAAGCTTATCTGTCTTGAATTTTAAAAAGTTGGGGGAGATTCTGAATTTGGTAAAGACATGCA  
 TGAATTTGGCTAAAAGAC-TGCA X 10 20  
 1620 1630 1640 1650 1660 1670 1680  
 TTTTAAACCTAGCAACTTATTTCTTTCTTTAAATAATCATAGCATTAATCCCAATCTTATTAAAG  
 TTTTAAACCTAGCAACTTATTTCTTTCTTTAAATAATCATAGCATTAATCCCAATCTTATTAAAG  
 30 40 50 60 70 80 90  
 1690 1700 1710 1720 1730 1740 1750  
 ACCCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGGTGTCTGTCTGTTACGTTTGAAGTC  
 ACCCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGGTGTCTGTCTGTTACGTTTGAAGTC  
 100 110 120 130 140 150 160  
 ACCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGGTGTCTGTCTGTTACGTTTGAANTC  
 1760 1770 1780 1790 1800 1810 1820 1830  
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGGAACACAGC  
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGGAACACAGC

170 180 190 200 210 220 230  
 1840 1850 1860 1870 1880 1890  
 GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGAAGGCTCATGGTGGACATGAAAGAGG  
 GCAGAAATGAAGGGCCAGGCTTACTGAGC-TGTCCAGTGAAGGCTCATGGTGGACATGAAAGAGG  
 240 250 260 270 280 290 300  
 1900 1910 1920 X 1930 1940 1950 1960 1970  
 CAGCTTAGGCCCCCTGGGGAGCCAGTCCACTGAGCAAGAGGACTGAGCCTTTTGCAGAAAGGCT  
 CAGCTTAGGCCCCCTGGGGAGCCCA  
 310 320 330 X

A

16. US-09-439-313-335 (1-2984)  
 US-09-159-812-20 Sequence 207, Application US/09159812A

Sequence 207, Application US/09159812A  
 Patent No. 6613872  
 GENERAL INFORMATION:  
 APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF  
 TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE  
 FILE REFERENCE: 210121.428C5  
 CURRENT APPLICATION NUMBER: US/09/159,812A  
 CURRENT FILING DATE: 1998-09-23  
 NUMBER OF SEQ ID NOS: 306  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 207  
 LENGTH: 332  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)..(332)  
 OTHER INFORMATION: n = A,T,C or G  
 Initial Score = 253 Optimized Score = 318 Significance = 1.84  
 Residue Identity = 96% Matches = 322 Mismatches = 7  
 Gaps = 4 Conservative Substitutions = 0

1550 1560 1570 1580 1590 X 1600 1610  
 CCCAAGCTTATCTGTCTTGAATTTTAAAAAGTTGGGGGAGATTCTGAATTTGGTAAAGACATGCA  
 TGAATTTGGCTAAAAGAC-TGCA X 10 20  
 1620 1630 1640 1650 1660 1670 1680  
 TTTTAAACCTAGCAACTTATTTCTTTCTTTAAATAATCATAGCATTAATCCCAATCTTATTAAAG  
 TTTTAAACCTAGCAACTTATTTCTTTCTTTAAATAATCATAGCATTAATCCCAATCTTATTAAAG  
 30 40 50 60 70 80 90  
 1690 1700 1710 1720 1730 1740 1750  
 ACCCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGGTGTCTGTCTGTTACGTTTGAAGTC  
 ACCCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGGTGTCTGTCTGTTACGTTTGAAGTC  
 100 110 120 130 140 150 160  
 ACCTACAGCTTGAAGAGTCACTACTGATTTATAGACCTTCTGGTGTCTGTCTGTTACGTTTGAANTC  
 1760 1770 1780 1790 1800 1810 1820 1830  
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGGAACACAGC  
 TGACATCTTGAAGATCTTTCATGACAGAGAGGTAAAGGATTTGATTTTCACAGAGGAACACAGC  
 170 180 190 200 210 220 230  
 GCAG-AATGAA-GGGCCAGGCTTACTGAGC-TGTCCAGTGAAGGCTCATGGTGGACATGAAAGAGG  
 GCAGAAATGAAGGGCCAGGCTTACTGAGC-TGTCCAGTGAAGGCTCATGGTGGACATGAAAGAGG

GCAGAAATGAGGGCCAGCTTACTAGCTTGTCCACTGAGGGCTCATGGTGGGACATGAGAAAGAGG  
 240 250 260 270 280 290 300  
 1900 1910 1920 X 1930 1940 1950 1960 1970  
 CAGCTTAGGCCCCCTGGGGAGCCCATGCTGACGACAGGAGGACTGAGTGAAGCCTTTTCAGAGAAAGGCT  
 310 320 330 X

A

17. US-09-439-313-335 (1-2984)  
 US-09-115-453-20 Sequence 207, Application US/09115453B

Sequence 207, Application US/09115453B  
 GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND  
 FILE REFERENCE: 210121.427C4  
 CURRENT APPLICATION NUMBER: US/09/115.453B  
 CURRENT FILING DATE: 1998-07-14  
 NUMBER OF SEQ ID NOS: 228  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 207  
 LENGTH: 332  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)...(332)  
 OTHER INFORMATION: n = A,T,C or G

Initial Score = 253 Optimized Score = 318 Significance = 1.84  
 Residue Identity = 96% Matches = 322 Mismatches = 7  
 Gaps = 4 Conservative Substitutions = 0

1550 1560 1570 1580 1590 X 1600 1610  
 CCCAAGCTTATCTGTCTTGTGACTTTTAAAAAGTTGGGGCAGATCTGAATGGCTTAAAAAGCATGCA  
 1620 1630 1640 1650 1660 1670 1680  
 TTTTAAAACTAGCACTTATTTCTTTCTTTTAAAAATACATAGCATTAATCCCAATCCTATTAAAG  
 30 40 50 60 70 80 90  
 TTTTAAAACTAGCACTTATTTCTTTCTTTTAAAAATACATAGCATTAATCCCAATCCTATTAAAG  
 1690 1700 1710 1720 1730 1740 1750  
 ACCGACAGCTTGAAGAGTCACTACATGCACTTTATAGACCTTCTGGTGTCTGCTTTAGCTTTGAATC  
 100 110 120 130 140 150 160  
 ACCGACAGCTTGAAGAGTCACTACATGCACTTTATAGACCTTCTGGTGTCTGCTTTAGCTTTGAATC  
 1760 1770 1780 1790 1800 1810 1820 1830  
 TGACATCTCTTGAATCTTTGATGACAGAGGAGTAAAGATTTGATTTTCAAGAGAAACACACAC  
 170 180 190 200 210 220 230  
 TGACATCTCTTGAATCTTTGATGACAGAGGAGTAAAGATTTGATTTTCAAGAGAAACACACAC  
 1840 1850 1860 1870 1880 1890 1900  
 GCAG-AATGAA-GGGCAGGCTTACTGAGC-TGTCCAGTGAAGGGGCTCAATGGTGGGACATGGAAGAGG  
 240 250 260 270 280 290 300  
 GCAGAAATGAGGGGCGAGCTTACTGAGCTGTCTCACTGGAGGGCTCATGGTGGGACATGGAAGAGG  
 1910 1920 X 1930 1940 1950 1960 1970  
 CAGCTTAGGCCCCCTGGGGAGCCCATGCTGACGACAGGAGGACTGAGTGAAGCCTTTTCAGAGAAAGGCT

CAGCTTAGGCCCCCTGGGGAGCCCA  
 310 320 330 X

A

18. US-09-439-313-335 (1-2984)  
 US-09-288-946-20 Sequence 207, Application US/09288946

Sequence 207, Application US/09288946  
 GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun  
 APPLICANT: Dillon, Davin C.  
 APPLICANT: Mitcham, Jennifer Lynn  
 TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS  
 FILE REFERENCE: 210121.427C7  
 CURRENT APPLICATION NUMBER: US/09/288,946  
 CURRENT FILING DATE: 1999-04-09  
 NUMBER OF SEQ ID NOS: 381  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 207  
 LENGTH: 332  
 TYPE: DNA  
 ORGANISM: Homo sapien  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)...(332)  
 OTHER INFORMATION: n = A,T,C or G

Initial Score = 253 Optimized Score = 318 Significance = 1.84  
 Residue Identity = 96% Matches = 322 Mismatches = 7  
 Gaps = 4 Conservative Substitutions = 0

1550 1560 1570 1580 1590 X 1600 1610  
 CCCAAGCTTATCTGTCTTGTGACTTTTAAAAAGTTGGGGCAGATCTGAATGGCTTAAAAAGCATGCA  
 1620 1630 1640 1650 1660 1670 1680  
 TTTTAAAACTAGCACTTATTTCTTTCTTTTAAAAATACATAGCATTAATCCCAATCCTATTAAAG  
 30 40 50 60 70 80 90  
 TTTTAAAACTAGCACTTATTTCTTTCTTTTAAAAATACATAGCATTAATCCCAATCCTATTAAAG  
 1690 1700 1710 1720 1730 1740 1750  
 ACCGACAGCTTGAAGAGTCACTACATGCACTTTATAGACCTTCTGGTGTCTGCTTTAGCTTTGAATC  
 100 110 120 130 140 150 160  
 ACCGACAGCTTGAAGAGTCACTACATGCACTTTATAGACCTTCTGGTGTCTGCTTTAGCTTTGAATC  
 1760 1770 1780 1790 1800 1810 1820 1830  
 TGACATCTCTTGAATCTTTGATGACAGAGGAGTAAAGATTTGATTTTCAAGAGAAACACACAC  
 170 180 190 200 210 220 230  
 TGACATCTCTTGAATCTTTGATGACAGAGGAGTAAAGATTTGATTTTCAAGAGAAACACACAC  
 1840 1850 1860 1870 1880 1890 1900  
 GCAG-AATGAA-GGGCAGGCTTACTGAGC-TGTCCAGTGAAGGGGCTCAATGGTGGGACATGGAAGAGG  
 240 250 260 270 280 290 300  
 GCAGAAATGAGGGGCGAGCTTACTGAGCTGTCTCACTGGAGGGCTCATGGTGGGACATGGAAGAGG  
 1910 1920 X 1930 1940 1950 1960 1970  
 CAGCTTAGGCCCCCTGGGGAGCCCATGCTGACGACAGGAGGACTGAGTGAAGCCTTTTCAGAGAAAGGCT

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360 370 380 390 400 410  
-GCAT-TACTCAC--TAAAG--GGC--TTCA--TTAGCCAGATTTTACTCTGGCTGACCTTACT  
TGAATGATATCCAGATGACAGCGGGCTGTTTGTATCACTCACTAAGA-GATTAAGCGTGATTTGATTTCTTT

1220	ATTGAGGCGCCAGCTTACTCTGTGGTGGCCAAATTTGCCAATATAGTTAATTAAGAGTGGCCCAATTCACCC	1230	1240	1250	1260	1270	1280
1220		1230	1240	1250	1260	1270	1280
1220	ACT-GAA-TATCAACT-CTG-----AAAGGCAAACTTAA--CAGAGAGAA--GGACAA-----	1230	1240	1250	1260	1270	1280
3410	3420	3430	3440	3450			
1290	1300	1310	1320	1330	1340	1350	1360
CCATTTCTGTGTGGCTCCACATTGCATGTCTAAATGCCACGTGCTGACACCGACCGAGTACTA							
CCA--GGATGAGAT--GTCACCA-AC TG-AAT--TAACTC							
3460	3470	3480	3490	3500			
GCCAGCACCAAGGCGAGGT							
1370	1380						

ATTTTCCTCCATGAAAGCGGTACGGCACTGGGGCTGGAGAGCATCTGGTCCGATTTGGGTACACCGCAATCGGCC	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300	4310	4320	4330	4340	4350	4360	4370	4380	4390	4400	4410	4420	4430	4440	4450	4460	4470	4480	4490	4500	4510	4520	4530	4540	4550	4560	4570	4580	4590	4600	4610	4620	4630	4640	4650	4660	4670	4680	4690	4700	4710	4720	4730	4740	4750	4760	4770	4780	4790	4800	4810	4820	4830	4840	4850	4860	4870	4880	4890	4900	4910	4920	4930	4940	4950	4960	4970	4980	4990	5000	5010	5020	5030	5040	5050	5060	5070	5080	5090	5100	5110	5120	5130	5140	5150	5160	5170	5180	5190	5200	5210	5220	5230	5240	5250	5260	5270	5280	5290	5300	5310	5320	5330	5340	5350	5360	5370	5380	5390	5400	5410	5420	5430	5440	5450	5460	5470	5480	5490	5500	5510	5520	5530	5540	5550	5560	5570	5580	5590	5600	5610	5620	5630	5640	5650	5660	5670	5680	5690	5700	5710	5720	5730	5740	5750	5760	5770	5
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TATTTCGCG-TTCCCCAAGCCTTATCTGCTGTGACTTTTAAAGTTGGGGCGAGTTCTGAAATTTGGG  
 TATGAGCTGGCGAGACAGTT-----TCCCGAC--TGGAAACGGCGAGATGGC--GCAACGCAATTAAT  
 2300 2310 2320 2330 2340 2350  
 540 550 560 570 580 590 600  
 CATAAAGA-CATGACATTTTAA--AACTAGGCACTTCTTATTTCTT--TTAAATACTATGACTTAA  
 GTTAAGTTAGCGGAATTTGCAACCAAGCGG--CATGCTGCTCCCACTTCGACATTTGGGGCGATGGA  
 2360 2370 2380 2390 2400 2410 2420  
 ATCCC--AAATCCTAT-TTAAAGACTTGAACGCTTGAGAAAG-TGACTACTGCAATTTATAGACTTTGCT  
 TGGCGGATAGCGCGCTGCTGGTTTCTTG--GATCCCGAGGATTTTGACCTGCGGTGAACCTCGCGAGGT  
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 680 690 700 710 720 730  
 GGTTCGTGCTTACGTTTGAAGTCTGA--CA-TCTCTTGAAATCTTTTGCATGCAAGAGAGTTAAG-----  
 GGTGAGC-CTCA-GGCAAGCAG-CTGAACCAACTGCGCAAGGGATC-GAGCCCGGGGTGG-GCGAAGACTC  
 2500 2510 2520 2530 2540 2550 2560  
 740 750 760 770 780 790 800  
 -GCTATTGATTTTACAGAGGAAGAACA--CAGGCGCAATGAAGGGCCAGGCTTACTGAGGCTGTCC----  
 CAGCATGAGATCCCGCGCTGAGGATCTATCCAGC-CGGCGTCCCGGAAGAAGATTCCGAAGCCCACTTTT  
 2570 2580 2590 2600 2610 2620 2630  
 810 820 830 840 850 860  
 AGTGAAGGGCTATGAGTGGAGCATGGA-----AGAAGGAGAGCTTAGG--CCCTGGGAGCCCACT-----  
 CATGAAGG--CGGCGGTGG--AAATGAAATCTCGTGAATGCGCAGGTGGGGCGTGGCTGTGCTGATTTGCA  
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 870 880 890 900 910 920  
 --CCACTGAG-CAAAC-AGA--GGAC--TGAGTAGCCTTTTGCAGGAAG--GCTAAGAAAAAGA-AAA  
 AACCACAAGTCCCTCAGAGAAGCTGCTCAAGAGGCGATGAAGAGCGAATGGCTTCGATCGGGGCGCG  
 2710 2720 2730 2740 2750 2760 2770  
 930 940 950 960 970 980 990  
 CCATTCT--TAAACACAAAGAAACTGTTC--CAATGTTGGGAAGCTGTGTTATATGC-CATAAATGGGT  
 CGATCCCGTAAAGCAC--GAGAGACGGGTCAAGCCATTGCGCGCCA-GCTCTTCA--GCAATATACGGGTG  
 2780 2790 2800 2810 2820 2830 2840  
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 CCCCAA-ATGSGGTAAAC--TGACTTCAAGAGAAATGAGCAGACCAAGCAAGAAATTTGGCTGTCTT  
 AGCCAAAGCTATGT--CTGATAGGCGTCCCGCAACCCAGCGCCGCAAGTCTGATGATCAGAAAAAGCGG  
 2850 2860 2870 2880 2890 2900 2910  
 1070 1080 1090 1100 1110 1120  
 CCATTTT-CATTCTGTATCTAGGTAGCTGTGTA-----GAGGGAGAC-ATTGAA--AAAAATGAACA  
 CCATTTTCCACCATATAT-TT-CGGCAAGCAGAGCATCGCAATGGGTGTACAGAGATCTTCGCGTGGGCA  
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 1130 1140 1150 1160 1170 1180  
 ACAAACAATTACTATAGAGTGAAGCTGAGGCTTGG--GAGTCTCTTGA--CTTCACTACTTAAT--TCCG  
 TGGCGGC-CTTAGGCTGGCGGAAGTTTCGG-CTGGCGGAG--CCCTGATGCTCTTGTGTCAGATCATTC-  
 2990 3000 3010 3020 3030 3040  
 1190 1200 1210 1220 1230 1240 1250  
 TTTTAGTGAAGAAC-ATTCAAT-----TTTCTT--TTATTGAAGGGCGAGCTTACTGTGTGGCAAAAT  
 -TGATGTGACAAAGACCGGCTTCAATCCGATCGAGTACGTCTCGCTCGA--TGGCAATGTTTCCCTGGTGTGCAAT  
 3050 3060 3070 3080 3090 3100 3110  
 TGGCA-ACATTAAG--TTATATGAAGAAGTTG--GCC-AAATTTAACC--CCATTTTCTGTGTGTTGGGCTTCACA

3. US-09-700-700-1 (1-1936)  
US-09-105-4708-2 Sequence 27, Application US/091054708

Initial Score	=	43	Optimized Score	=	182	Significance	=	1.29
Residue Identity	=	47%	Matches	=	253	Mismatches	=	158
Gaps	=	122	Conservative Substitutions	=	0			

1060 1070 1080 1090 1100 1110 1120 1130  
TTCCATTTCATTCTGTATCTCAGGTAGCTGTAGAGGGAGACATTAGAAAAAATGAAACAACAAAC  
GCTCGAGCT--TTCCAGCA---  
X 10

1140 1150 1160 1170 1180 1190 1200  
 AATTCTATAGGTACGCTGAGGCGCTGAGTCTCTTGACTCCACTATCTATTCCGTTGAGAAACC  
 AATCTCCAAAT AG -GGTT -GGTGG -CACACTCTGG -CTGA -GC -TTGG - - - - -CC

1210 1220 1230 1240 1250 1260 1270  
TTTCAATTTCTTTATTTAGAGGCGACGTTCTCTGTGGCAAAATGCCACATPA--GTTAATA-GA  
-----CTTGTCTTTTATAGA---GACACC---CTGGGAGAGC-AGTTTGAATCATTAAGTTTCACCT  
70 80 90 100 110 120

1280 1290 1300 1310 1320 1330 1340  
 AAGTGGCCCAATTACACCATTTCTGTGGTTGGCCGTCACATTCGAATTTCAATGCACACCGTGTGTG  
 GAGCTGGCC-ATT-ATC-AAAAGT-----GGGCTTCAC-TGCCACAG-CAGT-ACAGGTATGGCTTA  
 140 150 160 170 180

1350 1360 1370 1380 1390 1400 1410  
ACACCCGCGGAACTTATTCAGCCACACAATAAAGCAGGGTGCCTGAATCTTTCTGCTCTTACATTTCTTT  
GTAGAGTATCTCTTTATA-CACGGAACACAGGAGGCGCGGAGAA-GCC--CT-CTCTTT-CAGGCGCG

TAAATTAAGCATTTAATGCTCAGTCCCTACTAGATCTTTCTCTCCCTCTCTCAATTATTTCTTCA  
 1430 1440 1450 1460 1470 1480  
 CAAA--GAG---GATGCT--TCTCCA--AG-----TCTCCAGCTCCGAGGA--GACCTGCTTTC-  
 260 270 280 290

ACTCGAATTGGCAGGATTAACAACTTCACTGTGATTTATTT  
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AGCTTCATACCGCT---CTGTT-CTG-GAACCAAT-CTTCA-----CTTGCGGCTC

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|||GACCTGGAGAAAAATCATCTGAAGACTAGTCAATCAGCATCTGCAGGTAAATTG  
|||TGAACTT  
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ai Score	=	42	Optimized score	=	308	Significance	=	1.22
Identity	=	47%	Matches	=	415	Mismatches	=	268
	=	186	Conservative Substitutions	=				

560 570 580 590 600 X 610 620  
 AATACTGCGCACTTCTTATTTCTTCCCTTAAAAATACATAGCATTAACCAATCTCATTTAAAGC  
 ATGC-----TCAAGGTTCCGAG  
 X 10

530 640 650 660 670 680 690  
CTGACGCTTGAAGAAGTCACTACTGCAATTTATAGAACCTTCGTGCTTCCTGCTTACGTTTAAGTCG  
CGG-CGGCCCGGGAAG--CGAAGC--GAGGGGGCC--GCG--CCGCCACCCCGCTCCAAACCCG  
20 30 40 50 60 70

ACA-ATCTTGGAATCTTTG-CATGCGACAGAGAGTAAAGAGTATTGATTTGCACAGGAGAAAC--ACA  
 |||||  
 TCAAGTCTTCTTCATTCACGACATCTCGG-----GAGCGCGGCGACAGCGCAAGGCGGCGCGCACAGCA  
 80 90 100 110 120 130 140

GC-CAG--GACAGTSCG-----CCCGGAGCCGAGCGACGACGAGC-CA---GAAGG--GG-----  
150 160 170 180 190

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980 990 1000 1010 1020 1030 1040  
 GAGGCCGAGACCTGGCA--GAGCCGACCCAGA--GAGCAGCTTGGGCTTAT-CTGTGSA-CTGCG-  
 260 270 280 290 300 310

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-AAAACCT-TCAGCGCCCTTCCA---GGCTTCCCAAAACCC-  
 320 330 340 350 360 370  
 -AAACAG-CGCGAAGCGC

[illegible][illegible][illegible]

AAGCTAAGGAAA-----GCACTCTC-CTCGAGACTGGGAGCTTGG-----AGG-AGCACTCTCTTTTGC  
 540 550 560 570 580 590  
 1340 1350 1360 1370 1380 1390  
 CACCTGCTGTGACACCTGACCGGATAC-TGGCAGACACAAAGGACGGGTAGCC-TG---AATTGTTTCT

C---GGC-CCTGAA--GA--GGAGGCTTCTCCCGGC---CTCCCTGCTCTCCGCTATTAACGCTATTC  
 600 610 620 630 640 650  
 1400 1410 1420 1430 1440 1450 X 1460  
 GCCTTTACGTTCTT-TTTAAATTAAGCATTTAGTCTGATGCTCTTACGATGATCTTTCTCTCCCTCT

[illegible]



CTGAATTAA TTC TTTCAACTTGCAA TTGCAA

5. US-09-700-700-1 (1-1936)

US-09-105-470B-1 Sequence 1, Application US/09105470B

Initial Score =	42	Optimized Score =	308	Significance =	1.22
Residue Identifier =	47%	Matches =	415	Mismatches =	368

Gaps	=	186	Conservative Substitutions	=	0
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TTAAACTAGGCACTTCTTATTTCTTCTTCTTAAATAATAGCATTAATCCCAATCTATTTAAGAC

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**10**

630 640 650 660 670 680 690  
CTGACAGCTTTGAGAAGGTCACTACTGCAATTATTAAGGACCTTCTGGTGGTTTCTGCGTTAAGCTGTGG  
20 30 40 50 60 70  
CCG-CGGCCCGGGGAGG--GGAAGC--GGAGGGGACC----GCG--CCGCGACCCCGTCCAAAGCCGG

ACA -ATCTTGAGATCTTTG-CATGCAGACGGTAAGAAGTATTGTCAATTTTCACAGAGAAAGAAC--ACTC  
00           710       720       730       740       750       760

TGAGCTCTTCATCATCAGAACATCTCGCG-----GACGCGCGCGCACGCCGAAGCGCGCCGACGACGACG  
80           90       100       110       120       130       140

GC-CAGG-  
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840  
AGGAGCCTAGGCCCTTGGGAGGCCA--GTCCA-CTTAGCAACAAAGGACTACTGAGCTTTTGCAAGAA  
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ACGAGACC---GCCCGGGGCGCGAAGCAGACAGCTAGAGA---CCGAGCC---CCGCCCC---GGCGCGAAG  
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TTATGTGCTTAATGGGTC-CCAAATAGGTACTCTACCTTCAAGAAATGCGAGAGCGCAAGAGAA  
280 290 300 310 320 330 340 350 360 370  
-AAACA-CTTCAGGCGCCCTTCGA--GCTTCTCCCAAACTCC-----TAAGCAG-CCGCGAAGGCC  
330 340 350 360 370

[illegible]

TGAACACAAACAACTATCTAATAGAGTACGCTGAGCCCTGGAGGCTCTTAACTCCACTCTTAATTC  
 TTCAAGC--CATCAAGAGTAC--CTGTGGGCCCTCTGA--ACGGG--CCCACTCTGGC--CAAGAAGCTA--AA  
 430 440 450 460 470 480

TTTGTGAGAAACCTTTCATTTCTTTATTAAGAGGCGACTTCTGTGTGGCAAAATGCGACACAT  
CTCAGGAG-ACC---CAACT-----GAAG-----ATG-----TGGTTCGAGACAGCGCTA  
490 500 510 520 530

AAG-TTATAGAAAGTTGGCCAAATTCACCCCAATTTCTGTGGTTGGGCTCCACATGCAATGTCATATG

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AAAGCTAAGGAA----GCAGCTTC-CTCGAGCTGGGAGACTTGG-----AGA-AGCACTCCTCTTGC

1340 1350 1360 1370 1380 1390  
CAGCTGTGCTGACACCGAGATC-TAGCAGACAAAGCAGGTGAC-TG---AATGCTTCT  
C---GAC-CTTGAAA-GA-GGAGGCTTTCGGGAC---CTCCGCTCTCGGTATTAACGATATCC  
600 610 620 630 640 650

100 1410 1420 1430 1440 1450 X 1460  
GCTCTTACCACTTTCT-TTTAAATTAAGCAATTAGTGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCCT  
CTCTTTACCACTTTCT-TTTAAATTAAGCAATTAGTGTCTAGTCCCTACTGAGTACTCTTTCTCTCCCTCCTCCT  
TTTACTACCACTTACTGTACTGCTGGGCACTGAGCCACG---CTTTGGGTAA  
660 670 680 690 700 X

US-09-700-700-1 (1-1936)  
 00-10E 4700-2. Scanned by me/0910E4700  
 CTGATTTAATCTTTCACCTTGCAATTTGCAA  
 700 14800 1490 1500

Optimized Score =	229	Significance =	0.71
46% Matches =	294	Mismatches =	223
112 Conservative Substitutions =	0		

810 820 830 840 850 860 870  
 GGTAAAGAGATATGGATTTTCACAGAGAGAGAGACACATCGACAGAAATGAGGGCCAGGCTATCAGAGGCTGTG  
 NGCACAGC--AGNNAGGCACT-  
 X 10

880 890 900 910 920 930  
 ---TGAGGCTTATCTGTGTAACCTGTAACACTCTGAGGCGCTTCCAAAGCTTCCCAAAACCTTA  
 20 40 50 60 70 80

940 950 960 970 980 990 1000  
AGCAGCCGCAAAACCGCTCCGAG-CTGCCTTCTCCCACTCAGCTGATCGAGTTGGAGAGAGT-TCA

CCATCAGAACTACTCTC-----GGCCCTGGAAC-GGGCCCACTGGCCACAAG-----CTTCAG-----GCTCAG

1080 1090 1100 1110 1120 1130 1140  
 CACGAGAC-CCA AGCGAA-GATATGGTCCGACAGA-----CGCTATAAGACTA-AGCGAACAG--C  
 220 230 240 250 260 270

TCTCTCGGAGCT-----GGGAGAGC-TTGGA-----GAGC-ACGCTCTTTGACGGCCCTGGAGAG  
 280 290 300 310 320 330  
 1160 1170 1180 1190 1200 1210 1220

GGAGGCC-----NTTCNCCGGGCGNNC--CTGCTCNCCGTGTAT---AAC--AGCGA---NCTTANTAT  
1230 1240 1250 1260 1270 1280 1290  
340 350 360 370 380

CCCATACNTG-TAANGCNTGG-GGC---AANGGGAAGCCCACTTTTGTGTAANGGCCAGCTCA-----  
390 400 410 420 430 440

1300 1310 1320 1330 1340 1350 1360  
TTTGTGTTGGGCTCCACATGGAATGTCACGCGCTGCTACACCGACCGAGTACTAG--C  
-----GG--TGAACAC--CAT--AAGATCAA--AANG--GC--CTTNC--CCACGGGTGTTNATGAA  
450 460 470 480 490 500  
1370 1380 1390 X 1400 1410 1420 1430  
CAGCACAAGAGGAGGT--AGCCTGAATGCTTCTGCTTACATTTCTTTAAATAAGCATTTAGTCC  
|||||  
AAGCACAAGGGGCAAGTTCAGACCAAAAGN  
510 520 530 X  
1440  
TCAGTCCCT

7. US-09-700-700-1 (1-1936)  
US-09-105-470B-3 Sequence 30, Application US/09105470B

Initial Score = 33 Optimized Score = 152 Significance = 0.64  
Residue Identity = 52% Matches = 191 Mismatches = 115  
Gaps = 61 Conservative Substitutions = 0

780 790 800 810 820 X 830 840  
AAGATGAAGGGCCAGGCTTACTAGAGCTGTCCAGTGAAGGGCTCATAGGTGAGCAATGAAGAGGAGC  
|||||  
X GGGAGCTG--AGCCAG--AGC  
X 10

850 860 870 880 890 900 910  
CTAGGCGCTGGGAGCCAGTCCACTGAG--CA--AGCA--AGGAGTGAAGCTTGGCAGAAAAGGCT  
|||||  
C-AGAGCC--AGATCTCAGAACTGGGGTCTATGCTATAGAGCTGCCGA--CACTCTGAG--AG--CT  
20 30 40 50 60 70 80

920 930 940 950 960 970  
AAGAAAAAGG--AAACCATCTTAAACACAAAGAACTGCTCAATGCTTGGGAATGCTGTTATTT  
|||||  
CAGCGGCTGGGTCAACC-TTCTGGCACAC--TGCCACTGT--CGTTACTTTGG--CT--TTCTAGA  
90 100 110 120 130 140

980 990 1000 1010 1020 1030 1040  
GCTATTAATGGGCCCA--AAATGGTAACCTAGACTTACAGAGAAATGAGAGAGCAAGAGAAATC  
|||||  
GCC-AATATCTTGGCCATGAATGGTACTGCTTACTTCCAGGTAT--TTTGAGAAAGAG--TGAGATG  
150 160 170 180 190 200

1050 1060 1070 1080 1090 1100 1110  
TGGCTGCTCTTCAT--TTTCATCTGTTATCTCAGGTAGAGTGAAGGGA--GACATTAGAAAAAATGA  
|||||  
AAGTCAACGTATATATCTGTCGTTGCC--TGCCCTGCT--GTGGGGATGAC--AGATGATTTTG  
210 220 230 240 250 260 270

1120 1130 1140 1150 1160 1170 1180 1190  
AACACAAAAAATTAATTAATGAGTGAAGCTGAGGAGTCTTCTTCACTTCACTTAAATTCGGTT  
|||||  
GACAA--GACCAAGAGCT-----CGCTG--GGCATACTG--GTCTT--TCTTCAAG  
280 290 300 310 X

1200 1210 1220  
AGTGAGAAACCTTCAATTTCTTTATTGAAGG

8. US-09-700-700-1 (1-1936)  
US-09-105-470B-2 Sequence 26, Application US/09105470B

Initial Score = 28 Optimized Score = 54 Significance = 0.32  
Residue Identity = 50% Matches = 62 Mismatches = 50  
Gaps = 10 Conservative Substitutions = 0

1070 1080 1090 1100 1110 1120 1130 1140  
TTCTGTATCTCAGTGAAGCTGTAGAGGGAGACATTAGAAAAAATGAACAAACAAATTAATTAATG  
|||||

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AAGCTTAA--AATGCAAA--  
X 10

1150 1160 1170 1180 1190 1200 1210  
AGATAGGAGGCGCTGGAGTCTCTTGACTTCACTTAATTCGTTAGTGAACCTTTCAATTTTC  
|||||  
AATAGTTGA--CTTGTAG--CGATTA--CAATTAAGATGATCCCAATTTGTAG--CGATTAACAA--TTTC  
20 30 40 50 60 70 80

1220 1230 1240 1250 1260 1270 1280  
TTTATTAGAGGGCCAGCTTACTGTGTGTGCAAAATTTCCAAACATTAATTAAGAAAGTTGGCAATTT  
|||||  
ACACATTAAGAGAAATTAATTAATG  
90 100 110 X

1290  
CACCCC

9. US-09-700-700-1 (1-1936)  
US-09-105-470B-2 Sequence 28, Application US/09105470B

Initial Score = 25 Optimized Score = 219 Significance = 0.13  
Residue Identity = 46% Matches = 276 Mismatches = 221  
Gaps = 96 Conservative Substitutions = 0

410 420 430 440 450 460 470 480  
CCTAATTAAGCGCTTATTAATTAAGCCGAGATCTGTCTTTTNTGTTTTTTTTTTTCCCTCC  
|||||  
TTTTTTTCCCGCCAGCCCTCC  
X 10 20

490 500 510 520 530 540 550  
AAAGCTTATCTGCTTCTTCTTTTAAAGTTGGGGCAGATTTGAATTTGGCTTAAAGACATGATTT  
|||||  
GGAG--TTTAT--TC--ACTT--CCAGCGTACTGTGGCTG--GACCA--GCCTTGTGGCAT--CCGA  
30 40 50 60 70

560 570 580 590 600 610 620  
TTTAAACATGAGCAATCTTATTTCTTCTTTAAATTAATTAATTAATTAATTAATTAATTAAG  
|||||  
TTCAAGTCCA--GCAGCATCCAGTCTCT--ATCC--AGCATGGGGGACCCGCTGTCAAG  
80 90 100 110 120 130

630 640 650 660 670 680 690  
AAGTGAAGCTTGA--GAAGT--CACTACTGCATTTATAGACCTTCTGT--GTTTGTCTTTACCTTT  
|||||  
CTCTGGC--CTTCAGGAATCTTCGAGCTGCTCTTCTCTCGAAGTGGGGCTGGGCTCTG--GGTCCGCTT  
140 150 160 170 180 190 200

700 710 720 730 740 750 760  
GAACTGAACATCTTGAATCTT--TGCATGAG--AGAAGTGAAGAGTATTTGATTTTCAAGAGAAAG  
|||||  
-CTGGCT--CCAGTTCGGCTGTGTGTCTG--TTCAAGCTCGGTTCCAGCTGTGCTGGCTCG--GCTCC  
210 220 230 240 250 260 270

770 780 790 800 810 820 830  
AACACAGCGCAGAAATGAAGGGCCAGGCTTACTGAGGCTTCAATGAGAGGCTCATGGTGGACATGAA  
|||||  
GGTTCAAG--CTCTTTAGAGGCTCAAGCTTCCAG--CTGTG--GCTCCCG--GGGTCCG--  
280 290 300 310 320 330

840 850 860 870 880 890 900  
AAGAGGAGCTTGAAGCTCTGGGAGAGCCA--GTCCATGTCAGCAGCAGGAGTGAAGTCTTTTTCAGGA  
|||||  
-GATTCACCC--GCTTCGAGGCTGAGGCTCCGCTTCGCTCAAGTGAAGGTCTGA--AGC--TCG--GG--  
340 350 360 370 380 390

910 920 930 940 950 960 970  
AAGGCTTAAGAAAGAAACCATTTTAACACAAACAAAGAACTGTCAATGCTTTGGGAATGCTGTTT  
|||||  
CAACCGGGGCAATGTGTCAACGAGCGGGTGC--CTCC--GGGTCAAGTGGCTGGGATGAGAGGCTC  
|||||



17. US-09-700-700-1 (1-1936)  
US-09-105-4708-1 Sequence 17, Application US/091054708

Initial Score = 9 Optimized Score = 13 Significance = -0.90  
Residue Identity = 46% Matches = 13 Mismatches = 15  
Gaps = 0 Conservative Substitutions = 0

1530 1540 1550 1560 1570 1580 1590 1600  
ATTGTGTTGAGNGAGAAAAAGAAAGTCTTGTGTTAAATTAATCTGTTGTGATCATCTGCTTTT  
GCCGATCCCATGCTCAGGTT  
X  
10 20

1610 1620 1630 1640 1650  
CCCATTTGAACTAGTCAATTAACCACTCTGAACTGTAGAAAAACATCTGAGA  
CCGAG  
X

18. US-09-700-700-1 (1-1936)  
US-09-105-4708-2 Sequence 23, Application US/091054708

Initial Score = 8 Optimized Score = 8 Significance = -0.96  
Residue Identity = 53% Matches = 8 Mismatches = 7  
Gaps = 0 Conservative Substitutions = 0

1300 1310 1320 1330 1340 1350 1360  
TTTCTGTGTTGGGCTCCCAATGTGCAATGTTCATGCCACGCTGCTGACACCGAGGATGACTAGCCA  
ACACTTGTGAGGC  
X  
10 X

1370 1380 1390 1400  
GCACAAAAGCGAGGCTAGCTGAATGCTTCTGCTTTTACA

19. US-09-700-700-1 (1-1936)  
US-09-105-4708-2 Sequence 21, Application US/091054708

Initial Score = 8 Optimized Score = 13 Significance = -0.96  
Residue Identity = 54% Matches = 13 Mismatches = 11  
Gaps = 0 Conservative Substitutions = 0

820 830 840 850 860 870 880  
ATGGGTGGACATGAGAAAAAGGACAGCCTAGGCCCTGGGAGGCCAGTCACCTAGCAAGCAAGGACTGA  
CACTGCCAGTCACTGCTGCT  
X  
10 20

890 900 910 920 930  
GTGAGCCTTTTGCAGAAAAAGGCTAAGAAAAAGGAAACCATTTTAAACAC  
GA  
X



2050	2060	2070	2080	2090	2100	2110
350	360	370	380	390	400	
TG-TTGGCTCTCCCTAATGAT-TGGAGGT---CNGTA-----AATNCAAAACATATCCACTC						
TCCTTCATTTTCAITCTGTATCTCAGGTGAGCTGAGAGGGGAGACATTAGAAAAAATGAAACACAA						
2120	2130	2140	2150	2160	2170	2180
410	420	430	440	450	460	
AACACTT-CT--T---TTCNCGTA--NCT-TGANTCTGTATTCAGGA--NCAGCGGATGGAATGGGC						
AACATTTACTAATGAGTACGCTGAGGCTGGAGTCTCTTGACTCCACTTAATTCCG-TTAgTGAG-						
2190	2200	2210	2220	2230	2240	2250
470	480	X				
CAGCCNCGAGTGTCCANT						
AAACCTTTCAATTTCTTTTATTAGAAAGGCCACCTTACTGTGTGGCAAAATTGCCAAACATTAAGTTAA						
2260	2270	2280	2290	2300	2310	2320